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Output Set: N:\CRF3\09042001\I612914A.raw

SEQUENCE LISTING

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4 (1) GENERAL INFORMATION:
                                                                 unhuato
      6
             (i) APPLICANT: Hanna, Nabil
     .7
                            Newman, Roland A.
      8
                            Reff, Mitchell E.
            (ii) TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies
     10
     11
                                      Therapy
     13
           (iii) NUMBER OF SEQUENCES: 59
     15
            (iv) CORRESPONDENCE ADDRESS:
                  (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
     16
                  (B) STREET: 699 Prince Street
     17
                  (C) CITY: Alexandria
     18
                                                           ENTERED
     19
                  (D) STATE: VA
     20
                  (E) COUNTRY: USA
     21
                  (F) ZIP: 22314-3187
     23
             (v) COMPUTER READABLE FORM:
     24
                  (A) MEDIUM TYPE: Floppy disk
                  (B) COMPUTER: IBM PC compatible
     25
     26
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     27
            (vi) CURRENT APPLICATION DATA:
     29
                  (A) APPLICATION NUMBER: US/09/612,914A
C--> 30
                  (B) FILING DATE: 10-Jul-2000
C--> 31
     37
                  (C) CLASSIFICATION:
     34
           (vii) PRIOR APPLICATION DATA:
     35
                  (A) APPLICATION NUMBER: US 08/523,894
                  (B) FILING DATE: 06-SEP-1995
     36
          (viii) ATTORNEY/AGENT INFORMATION:
     39
     40
                  (A) NAME: Teskin, Robin L.
                  (B) REGISTRATION NUMBER: 35,030
     41
     42
                  (C) REFERENCE/DOCKET NUMBER: 012712-165
            (ix) TELECOMMUNICATION INFORMATION:
     44
     45
                  (A) TELEPHONE: 703-836-6620
                  (B) TELEFAX: 703-836-2021
     46
     49
        (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     51
     52
                  (A) LENGTH: 420 base pairs
     53
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: single
     54
     55
                  (D) TOPOLOGY: linear
     57
            (ii) MOLECULE TYPE: DNA (genomic)
     59
            (vi) ORIGINAL SOURCE:
     60
                  (A) ORGANISM: Monkey
     62
          (viii) POSITION IN GENOME:
     63
                  (A) CHROMOSOME/SEGMENT: light variable domain of CE9.1
     65
            (ix) FEATURE:
     66
                  (A) NAME/KEY: CDS
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67 (B) LOCATION: 4420	
69 (ix) FEATURE:	
70 (A) NAME/KEY: mat_peptide	
71 (B) LOCATION: 61420	
74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	48
76 GAC ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA	40
77 Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg	
78 -19 -15 -10 -5	96
80 TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG	96
81 Trp Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val	
82 1 5 10 mg/s are seen as a mg/s are seen are seen a mg/s are seen are seen a mg/s are seen are seen are seen are seen are see	1 4 4
84 AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC	144
85 Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser	
86 15 20 25	100
88 ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG	192
89 Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys	
.90 30 35 40	240
92 GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT	240
93 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn	
94 45 50 55 60	200
96 TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC	288
97 Tyr Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser	
98 65 70 75	226
100 AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG	. 336
101 Lys Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr	
102 80 85 90	204
104 GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA	384
105 Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu	
106 95 100 105	420
108 TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC	420
109 Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser	
110 110 115 120	
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115 (i) SEQUENCE CHARACTERISTICS:	
116 (A) LENGTH: 139 amino acids	
117 (B) TYPE: amino acid	
118 (D) TOPOLOGY: linear	
120 (ii) MOLECULE TYPE: protein	
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127 Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val Lys	
128 1 5 10	
130 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile	•
131 15 20 25	
133 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly	
134 30 35 40 45	
136 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr	
137 50 55 60	

139																	
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140				65					70			_	_	75			
142	Asn	Leu	Phe	Ser	Leu	Lys	Leu		Ser	Val	Thr	Ala		Asp	Thr	Ala	
143			80					85					90		_	_	
145	Val	Tyr	Tyr	Cys	Àla	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	Leu	
146		95					100					105					
148	Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser						
149	110					115					120						•
151	(2)	INFO	RMAI	NOI	FOR	SEQ	ID N	10: 3	3:								
153		(i)	SEÇ	UENC	E CF	IARAC	TER	STIC	CS:								
154			(A) LE	NGTH	1: 38	37 ba	se p	pairs	3							
155			(E	3) TY	PE:	nucl	leic	acid	ì								
156			(0	C) SI	RANI	DEDNE	ESS:	sing	jle								
157			(I) TC	POLO	OGY:	line	ear									
159		(ii)	MOI	ECUI	E TY	PE:	DNA	(ger	nomio	2)							
161		(vi)	ORI	GINA	AL SO	OURCE	Ξ:										
162						ISM:		сеу									
164	7)	/iii)	POS	İTIC	I NO	N GEI	NOME	;									
165	•								r: he	eavy	var	iable	e dor	nain	of (CE9.1	
167		(ix)	FE <i>P</i>	-													
168						KEY:	CDS										
169				•		ION:		387									
171		(ix)	, FE <i>P</i>	•													
172		(=== .				KEY:	mat	pept	tide								
173			•	•	•	ION:											
176		(xi	SEÇ						SEQ :	ID N) : 3	:					
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179		Met	Ala	Trp	Ala	Leu	Leu	Leu	ьeu	GIY	Leu	ьeu	Ala	HlS	Phe	Thr	
179 180		Met	Ala	Trp	Ala	Leu -15	Leu	Leu	ьeu	GIY	Leu -10	ьeu	Ala	HIS	Phe	Thr -5	
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180 182	GAC Asp	Met -19 TCT	Ala GCG	Trp GCC	Ala TCC	Leu -15 TAT	GAG	TTG	AGT	CAG	-10 CCT	CGC	TCA	GTG	TCC	-5 GTG	96
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180 182 183 184	Asp	Met -19 TCT Ser	Ala GCG Ala	Trp GCC Ala	Ala TCC Ser 1	Leu -15 TAT Tyr	GAG Glu	TTG Leu	AGT Ser 5	CAG Gln	-10 CCT Pro	CGC Arg	TCA Ser	GTG Val 10	TCC Ser	-5 GTG Val	96 144
180 182 183 184 186	Asp TCC	Met -19 TCT Ser	Ala GCG Ala GGA	Trp GCC Ala CAG	TCC Ser 1 ACG	Leu -15 TAT Tyr	GAG Glu GGG	TTG Leu TTC	AGT Ser 5 ACC	CAG Gln	-10 CCT Pro	CGC Arg	TCA Ser	GTG Val 10 AAC	TCC Ser	-5 GTG Val	
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180 182 183 184 186 187 188	Asp TCC Ser	Met -19 TCT Ser CCA Pro	Ala GCG Ala GGA Gly 15	Trp GCC Ala CAG Gln	TCC Ser 1 ACG Thr	Leu -15 TAT Tyr GCC Al`a	GAG Glu GGG Gly	TTG Leu TTC Phe 20	AGT Ser 5 ACC Thr	CAG Gln TGT Cys	-10 CCT Pro GGG Gly	CGC Arg GGA Gly	TCA Ser GAC Asp 25	GTG Val 10 AAC Asn	TCC Ser GTT Val	-5 GTG Val GGA Gly	
180 182 183 184 186 187 188 190	Asp TCC Ser	Met -19 TCT Ser CCA Pro	Ala GCG Ala GGA Gly 15 AGT	Trp GCC Ala CAG Gln GTA	TCC Ser 1 ACG Thr	Leu -15 TAT Tyr GCC Ala	GAG Glu GGG Gly TAC	TTG Leu TTC Phe 20 CAG	AGT Ser 5 ACC Thr	CAG Gln TGT Cys	-10 CCT Pro GGG Gly CCA	CGC Arg GGA Gly CCG	TCA Ser GAC Asp 25 CAG	GTG Val 10 AAC Asn	TCC Ser GTT Val	-5 GTG Val GGA Gly GTG	144
180 182 183 184 186 187 188 190	TCC Ser AGG Arg	Met -19 TCT Ser CCA Pro AAA Lys	Ala GCG Ala GGA Gly 15 AGT	Trp GCC Ala CAG Gln GTA	TCC Ser 1 ACG Thr	Leu -15 TAT Tyr GCC Ala	GAG Glu GGG Gly TAC	TTG Leu TTC Phe 20 CAG	AGT Ser 5 ACC Thr	CAG Gln TGT Cys	-10 CCT Pro GGG Gly CCA	CGC Arg GGA Gly	TCA Ser GAC Asp 25 CAG	GTG Val 10 AAC Asn	TCC Ser GTT Val	-5 GTG Val GGA Gly GTG	144
180 182 183 184 186 187 188 190 191	TCC Ser AGG Arg	Met -19 TCT ser CCA Pro AAA Lys 30	GCG Ala GGA Gly 15 AGT Ser	Trp GCC Ala CAG Gln GTA Val	TCC Ser 1 ACG Thr CAG Gln	Leu -15 TAT Tyr GCC Ala TGG	GAG Glu GGG Gly TAC Tyr 35	TTG Leu TTC Phe 20 CAG Gln	AGT Ser 5 ACC Thr CAG Gln	CAG Gln TGT Cys AAG Lys	-10 CCT Pro GGG Gly CCA Pro	CGC Arg GGA Gly CCG Pro 40	TCA Ser GAC Asp 25 CAG Gln	GTG Val 10 AAC Asn GCC Ala	TCC Ser GTT Val CCT Pro	-5 GTG Val GGA Gly GTG Val	144
180 182 183 184 186 187 188 190 191 192	TCC Ser AGG Arg	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC	Ala GCG Ala GGA Gly 15 AGT Ser	Trp GCC Ala CAG Gln GTA Val	Ala TCC Ser 1 ACG Thr CAG Gln GCT	Leu -15 TAT Tyr GCC Ala TGG Trp	GAG Glu GGG Gly TAC Tyr 35 AGC	TTG Leu TTC Phe 20 CAG Gln	AGT Ser 5 ACC Thr CAG Gln	CAG Gln TGT Cys AAG Lys	-10 CCT Pro GGG Gly CCA Pro	CGC Arg GGA Gly CCG Pro 40 GGG	TCA Ser GAC Asp 25 CAG Gln	GTG Val 10 AAC Asn GCC Ala	TCC Ser GTT Val CCT Pro	-5 GTG Val GGA Gly GTG Val	144
180 182 183 184 186 187 188 190 191 192 194 195	TCC Ser AGG Arg CTG Leu	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC	Ala GCG Ala GGA Gly 15 AGT Ser	Trp GCC Ala CAG Gln GTA Val	Ala TCC Ser 1 ACG Thr CAG Gln GCT	Leu -15 TAT Tyr GCC Ala TGG Trp GAC Asp	GAG Glu GGG Gly TAC Tyr 35 AGC	TTG Leu TTC Phe 20 CAG Gln	AGT Ser 5 ACC Thr CAG Gln	CAG Gln TGT Cys AAG Lys	-10 CCT Pro GGG Gly CCA Pro	CGC Arg GGA Gly CCG Pro 40	TCA Ser GAC Asp 25 CAG Gln	GTG Val 10 AAC Asn GCC Ala	TCC Ser GTT Val CCT Pro	-5 GTG Val GGA Gly GTG Val	144
180 182 183 184 186 187 188 190 191 192 194 195	TCC Ser AGG Arg CTG Leu 45	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC Val	Ala GCG Ala GGA Gly 15 AGT Ser ATC	Trp GCC Ala CAG Gln GTA Val TAT Tyr	TCC Ser 1 ACG Thr CAG Gln GCT Ala	Leu -15 TAT Tyr GCC Ala TGG Trp GAC Asp 50	GAG Glu GGG Gly TAC Tyr 35 AGC Ser	TTG Leu TTC Phe 20 CAG Gln GAA Glu	AGT Ser 5 ACC Thr CAG Gln CGG Arg	CAG Gln TGT Cys AAG Lys CCC Pro	-10 CCT Pro GGG Gly CCA Pro TCA Ser 55	CGC Arg GGA Gly CCG Pro 40 GGG Gly	TCA Ser GAC Asp 25 CAG Gln ATC Ile	GTG Val 10 AAC Asn GCC Ala CCT Pro	TCC Ser GTT Val CCT Pro GCG Ala	-5 GTG Val GGA Gly GTG Val CGA Arg 60	144
180 182 183 184 186 187 188 190 191 192 194 195 196	TCC Ser AGG Arg CTG Leu 45	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC Val	Ala GCG Ala GGA Gly 15 AGT Ser ATC Ile GGC	Trp GCC Ala CAG Gln GTA Val TAT Tyr TCC	TCC Ser 1 ACG Thr CAG Gln GCT Ala	Leu -15 TAT Tyr GCC Ala TGG Trp GAC Asp 50 TCA	GAG Glu GGG Gly TAC Tyr 35 AGC Ser	TTG Leu TTC Phe 20 CAG Gln GAA Glu	AGT Ser 5 ACC Thr CAG Gln CGG Arg	CAG Gln TGT Cys AAG Lys CCC Pro	-10 CCT Pro GGG Gly CCA Pro TCA Ser 55 ACC	CGC Arg GGA Gly CCG Pro 40 GGG Gly	TCA Ser GAC Asp 25 CAG Gln ATC Ile	GTG Val 10 AAC Asn GCC Ala CCT Pro	TCC Ser GTT Val CCT Pro GCG Ala	-5 GTG Val GGA Gly GTG Val CGA Arg 60 GGG	144 192 240
180 182 183 184 186 187 188 190 191 192 194 195 196 198	TCC Ser AGG Arg CTG Leu 45	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC Val	Ala GCG Ala GGA Gly 15 AGT Ser ATC Ile GGC	Trp GCC Ala CAG Gln GTA Val TAT Tyr TCC	TCC Ser 1 ACG Thr CAG Gln GCT Ala AAC	Leu -15 TAT Tyr GCC Ala TGG Trp GAC Asp 50 TCA	GAG Glu GGG Gly TAC Tyr 35 AGC Ser	TTG Leu TTC Phe 20 CAG Gln GAA Glu	AGT Ser 5 ACC Thr CAG Gln CGG Arg	CAG Gln TGT Cys AAG Lys CCC Pro	-10 CCT Pro GGG Gly CCA Pro TCA Ser 55 ACC	CGC Arg GGA Gly CCG Pro 40 GGG Gly	TCA Ser GAC Asp 25 CAG Gln ATC Ile	GTG Val 10 AAC Asn GCC Ala CCT Pro	TCC Ser GTT Val CCT Pro GCG Ala	-5 GTG Val GGA Gly GTG Val CGA Arg 60 GGG	144 192 240
180 182 183 184 186 187 188 190 191 192 194 195 196 198 199 200	TCC Ser AGG Arg CTG Leu 45 TTC Phe	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC Val TCT Ser	Ala GCG Ala GGA Gly 15 AGT Ser ATC Ile GGC Gly	Trp GCC Ala CAG Gln GTA Val TAT Tyr TCC Ser	TCC Ser 1 ACG Thr CAG Gln GCT Ala AAC Asn 65	Leu -15 TAT Tyr GCC Ala TGG Trp GAC Asp 50 TCA Ser	GAG Glu GGG Gly TAC Tyr 35 AGC Ser GGG Gly	TTG Leu TTC Phe 20 CAG Gln GAA Glu AAC Asn	AGT Ser 5 ACC Thr CAG Gln CGG Arg ACC	CAG Gln TGT Cys AAG Lys CCC Pro GCC Ala 70	-10 CCT Pro GGG Gly CCA Pro TCA Ser 55 ACC Thr	CGC Arg GGA Gly CCG Pro 40 GGG Gly CTG Leu	TCA Ser GAC Asp 25 CAG Gln ATC Ile ACC Thr	GTG Val 10 AAC Asn GCC Ala CCT Pro	TCC Ser GTT Val CCT Pro GCG Ala AGC Ser 75	GTG Val GGA Gly GTG Val CGA Arg 60 GGG Gly	144 192 240
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180 182 183 184 186 187 188 190 191 192 194 195 196 198 199 200 202 203	TCC Ser AGG Arg CTG Leu 45 TTC Phe	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC Val TCT Ser	Ala GCG Ala GGA Gly 15 AGT Ser ATC Ile GGC Gly GCC	Trp GCC Ala CAG Gln GTA Val TAT Tyr TCC Ser GGG Gly	TCC Ser 1 ACG Thr CAG Gln GCT Ala AAC Asn 65 GAT	Leu -15 TAT Tyr GCC Ala TGG Trp GAC Asp 50 TCA Ser	GAG Glu GGG Gly TAC Tyr 35 AGC Ser GGG Gly	TTG Leu TTC Phe 20 CAG Gln GAA Glu AAC Asn	AGT Ser 5 ACC Thr CAG Gln CGG Arg ACC Thr	CAG Gln TGT Cys AAG Lys CCC Pro GCC Ala 70 TAC	-10 CCT Pro GGG Gly CCA Pro TCA Ser 55 ACC Thr	CGC Arg GGA Gly CCG Pro 40 GGG Gly CTG Leu	TCA Ser GAC Asp 25 CAG Gln ATC Ile ACC Thr	GTG Val 10 AAC Asn GCC Ala CCT Pro ATC Ile	TCC Ser GTT Val CCT Pro GCG Ala AGC Ser 75 GAC	GTG Val GGA Gly GTG Val CGA Arg 60 GGG Gly AGT	144 192 240 288
180 182 183 184 186 187 188 190 191 192 194 195 196 198 199 200 202 203 204	TCC Ser AGG Arg CTG Leu 45 TTC Phe	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC Val TCT ser GAG Glu	Ala GCG Ala GGA Gly 15 AGT Ser ATC Ile GGC Gly GCC Ala	Trp GCC Ala CAG Gln GTA Val TAT Tyr TCC Ser GGG Gly 80	TCC Ser 1 ACG Thr CAG Gln GCT Ala AAC Asn 65 GAT Asp	Leu -15 TAT Tyr GCC Ala TGG Trp GAC Asp 50 TCA ser GAG Glu	GAG Glu GGG Gly TAC Tyr 35 AGC Ser GGG Gly GCT Ala	TTG Leu TTC Phe 20 CAG Gln GAA Glu AAC Asn	AGT Ser 5 ACC Thr CAG Gln CGG Arg ACC Thr TAT Tyr 85	CAG Gln TGT Cys AAG Lys CCC Pro GCC Ala 70 TAC Tyr	-10 CCT Pro GGG Gly CCA Pro TCA Ser 55 ACC Thr	CGC Arg GGA Gly CCG Pro 40 GGG Gly CTG Leu CAG Gln	TCA Ser GAC Asp 25 CAG Gln ATC Ile ACC Thr	GTG Val 10 AAC Asn GCC Ala CCT Pro ATC Ile TGG Trp 90	TCC Ser GTT Val CCT Pro GCG Ala AGC Ser 75 GAC Asp	GTG Val GGA Gly GTG Val CGA Arg 60 GGG Gly AGT Ser	144 192 240 288 336
180 182 183 184 186 187 188 190 191 192 194 195 196 198 199 200 202 203 204 206	ASP TCC Ser AGG Arg CTG Leu 45 TTC Phe GTC Val	Met -19 TCT Ser CCA Pro AAA Lys 30 GTC Val TCT ser GAG Glu	Ala GCG Ala GGA Gly 15 AGT Ser ATC Ile GGC Gly GCC Ala	Trp GCC Ala CAG Gln GTA Val TAT Tyr TCC Ser GGG Gly 80 CAT	TCC Ser 1 ACG Thr CAG Gln GCT Ala AAC Asn 65 GAT Asp	Leu -15 TAT Tyr GCC Ala TGG Trp GAC Asp 50 TCA Ser GAG Glu GTC	GAG Glu GGG Gly TAC Tyr 35 AGC Ser GGG Gly GCT Ala	TTG Leu TTC Phe 20 CAG Gln GAA Glu AAC Asn GAC Asp	AGT Ser 5 ACC Thr CAG Gln CGG Arg ACC Thr TAT Tyr 85 GGA	CAG Gln TGT Cys AAG Lys CCC Pro GCC Ala 70 TAC Tyr	-10 CCT Pro GGG Gly CCA Pro TCA Ser 55 ACC Thr TGT Cys	CGC Arg GGA Gly CCG Pro 40 GGG Gly CTG Leu CAG Gln CGG	TCA Ser GAC Asp 25 CAG Gln ATC Ile ACC Thr GTG Val	GTG Val 10 AAC Asn GCC Ala CCT Pro ATC Ile TGG Trp 90 ACC	TCC Ser GTT Val CCT Pro GCG Ala AGC Ser 75 GAC Asp	GTG Val GGA Gly GTG Val CGA Arg 60 GGG Gly AGT	144 192 240 288

208 210 GGT	95	100		105	387						
210 GG1											
_	INFORMATION FOR	SEO ID NO. 4.									
217	(i) SEQUENCE CH		•								
218	• •	: 128 amino a									
219	• •		CIUS								
220	(B) TYPE: amino acid(D) TOPOLOGY: linear										
222	(ii) MOLECULE TY										
224	(xi) SEQUENCE DE	-	O TD NO. 4.								
	Ala Trp Ala Leu			His Phe Thr Asp							
227 -19		Dea Dea Dea e.	-10	-5							
	Ala Ala Ser Tyr	Glu Leu Ser G	- -	_							
230	1	5		10							
	Gly Gln Thr Ala	Gly Phe Thr C	vs Gly Gly Asp	Asn Val Gly Arg							
233	15	20	25	•							
235 Lys	Ser Val Gln Trp	Tyr Gln Gln L	ys Pro Pro Gln	Ala Pro Val Leu							
236 30	_	35	40	45							
238 Val	Ile Tyr Ala Asp	Ser Glu Arg P:	ro Ser Gly Ile	Pro Ala Arg Phe							
239	50		55	60							
241 Ser	Gly Ser Asn Ser.	Gly Asn Thr A	la Thr Leu Thr	Ile Ser Gly Val							
242	65	•	70	· 75							
244 Glu	Ala Gly Asp Glu	Ala Asp Tyr T	yr Cys Gln Val	Trp Asp Ser Thr							
245	80	85		90							
	Asp His Trp Val			Thr Val Leu Gly							
248	95	100	105								
• •	INFORMATION FOR										
253	(i) SEQUENCE CH										
254	• •	: 702 base pa:	ırs								
255	• •	nucleic acid									
256	• •	EDNESS: single	е								
257 259	• •	GY: linear	mia)								
261	(ii) MOLECULE TY (vi) ORIGINAL SO		mile)								
262	•	SM: Homo sapi	enc								
	viii) POSITION IN	_	CIID								
265	· · · · · · · · · · · · · · · · · · ·		lambda variabl	Le and constant doma	ins in						
266	(11)		CE9.1								
268	(ix) FEATURE:		,								
269	(A) NAME/K	EY: CDS									
270	, ,	ON: 1702									
272	(ix) FEATURE:										
273		EY: mat_peption	de								
274	(B) LOCATI	ON: 1702									
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279 ATG	GCC TGG GCT CTG	CTG CTC CTC G	GC CTC CTT GCT	CAC TTT ACA GAC	48						
280 Met	Ala Trp Ala Leu	Leu Leu Leu G	ly Leu Leu Ala	His Phe Thr Asp							
281 1			10	15							
283 TCT	GCG GCC TCC TAT	GAG TTG AGT C	AG CCT CGC TCA	GTG TCC GTG TCC	96						

RAW SEQUENCE LISTING

DATE: 09/04/2001

PATENT APPLICATION: US/09/612,914A TIME: 12:34:34

	•										_	1		*** 1	C	
284 Ser	Ala	Ala	Ser	Tyr	Glu	Leu	Ser		Pro.	Arg	Ser	vaı	ser	vaı	ser	
285			20					25		223	C 3 C	220	30	CCA	NGG	144
287 CCA	GGA	CAG	ACG	GCC	GGG	TTC	ACC	TGT	GGG	GGA	Agn	AAC	U = 1	GGA	Arα	744
288 Pro	Gly		Thr	Ala	Gly	Phe		Cys	GIY	GIY	ASP	45	vaı	GIY	AT 9	
289		35				~ ~	40	220	CC3	ccc	CAG		ССТ	GTG	CTG	192
291 AAA	AGT	GTA	CAG	TGG	TAC	CAG	CAG	AAG	Dro	Dro	Cln	λla	Pro	Val	Leu	
292 Lys		Val	GIn	Trp	туг	55	GIII	гу	PIO	FIO	60	niu	110			
293 295 GTC	50	mam	com	CAC	NCC		ccc	CCC	тса	GGG		ССТ	GCG	CGA	TTC	240
295 GTC 296 Val	ATC	TAT	Ala	Acn	Sar	Glu	Δrσ	Pro	Ser	Glv	Ile	Pro	Ala	Arg	Phe	
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297 65 299 TCT	ccc	ጥርር	ממכ	ΨСА	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AGC	GGG	GTC	288
300 Ser	Glv	Ser	Asn	Ser	Glv	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Val	
300 361	GIY	501		85					90					95		
303 GAG	GCC	GGG	GAT	GAG	GCT	GAC	TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGT	ACT	336
304 Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ser	Thr	
305			100					105					110			
307 ርርጥ	GAT	CAT	TGG	GTC	TTC	GGC	GGA	GGG	ACC	CGG	CTG	ACC	GTC	CTA	GGT	384
308 Ala	Asp	His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr	Val	Leu	Gly	
309		115					120					125				422
311 CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	GAG	. 432
312 Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	GIU	
313	130					135					140					480
315 GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	A'l'A	AGT	GAC	TTC	400
316 Glu	Leu	Gln	Ala	Asn		Ala	Thr	Leu	Val	Cys	ьeu	ire	ser	ASP	160	
317 145					150					155		7.00	7.00	CCC		. 528
319 TAC	CCG	GGA	GCC	GTG	ACA	GTG	GCC	TGG	AAG	GCA	AAT	AGC	Car	Pro	Val	. 320
320 Tyr	Pro	Gly	Ala		Thr	vaı	Ala	Trp	ьуs 170	Ala	изр	261	JCI	175	val	
321				165	3.00	3.00	አ ረግ አ	CCC			$C\Delta\Delta$	AGC	AAC	-		576
323 AAG 324 Lys	GCG	GGA	GTG	GAG	ACC	Mhr	Thr	Pro	Ser	Lvs	Gln	Ser	Asn	Asn	Lys	
	Ala	GIY	180		1111	T 11T	T 111	185		шу	02		190		-	
325 327 TAC	CCC	CCC	100	ACC	ጥልሮ	CTG	AGC			CCI	GAG	CAG	TGG	AAG	TCC	624
327 TAC 328 Tyr	λla	λla	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	
320 TYL 329	Ала	195		001	-1-		200					205	_			
331 CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAI	GAA	GGG	AGC	ACC	GTG	GAG	672
332 His	Ara	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	ı Gly	Ser	Thr	Val	Glu	
333	210		-		_	215					220)				
335 AAG		GTG	GCC	CCT	ACA	GAA	TGT	TCA	TGA							702
336 Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	•							
337 225					230	l										
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/612,914A

DATE: 09/04/2001 TIME: 12:34:35

Input Set : N:\Crf3\RULE60\09612914A.txt Output Set: N:\CRF3\09042001\I612914A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]